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<110> Arkowitz, Robert A
Nern, Peter MA

<120> NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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<141> 2002-01-21

<150> 09/168,474
<151> 1998-10-08

<150> 08/951,141
<151> 1997-10-15

<150> 09/529,106
<151> 2000-04-07

<150> US 09/732,180
<151> 2000-12-07

<150> US 60/169,699
<151> 1999-12-07

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
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<210> 2
<211> 76
<212> PRT
<213> Saccharomyces cerevisiae

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 1               5                  10                  15
Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
            20                  25                  30
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Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
        35                  40                  45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
    50                  55                  60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65                  70                  75
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<210> 3
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<212> DNA
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<220>
<223> cdc24-m1

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
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<213> Artificial Sequence

<220>
<223> cdc24-m1

<400> 4
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 1               5                  10                  15
Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
            20                  25                  30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
        35                  40                  45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
    50                  55                  60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65                  70                  75
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<223> cdc24-m2

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctggtca aagtgctaga agtagtagaa acgctaatga attccagc              228
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<210> 6
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> cdc24-m2

<400> 6
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 1   5   10   15
Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
            20   25   30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
        35   40   45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
    50   55   60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65   70   75

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<213> Artificial Sequence

<220>
<223> cdc24-m3

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gacgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaacac 120
tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
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<212> PRT
<213> Artificial Sequence

<220>
<223> cdc24-m3

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            20   25   30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
        35   40   45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
    50   55   60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65   70   75

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<213> Artificial Sequence

<220>
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Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
        35   40   45
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
    50   55   60
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
65   70   75   80
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
                85   90   95
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
            100   105   110
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
        115   120   125
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
    130   135   140
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
145   150   155   160
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
                165   170   175
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
            180   185   190
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe
        195   200   205
Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg
    210   215   220
Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu
225   230   235   240
Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser
                245   250   255
Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly
            260   265   270
Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser
        275   280   285
Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser
    290   295   300
Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser
305   310   315   320
Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
                325   330   335
Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
            340   345   350
Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
        355   360   365
Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
    370   375   380
Gln Leu Ile His Asp Leu Lys Asn

385 390

<210> 10
<211> 1269
<212> DNA
<213> Saccharomyces cerevisiae

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gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaca caagatacaa 180
gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
ttaaagccaa atatcgtgtt gaaaggccat aataataaaa tctcagattt tcggtggagt 300
cgagattcaa aacgtatttt gagtgcaagt caagatggct ttatgcttat atgggacagt 360
gcttcaggtt taaaacagaa cgctattcca ttagattctc aatgggttct ttcctgcgct 420
atttcgccat cgagtacttt ggtagcaagc gcaggattaa acaataactg taccatttat 480
agagtttcga aagaaaacag agtagcgcaa aacgttgcgt caatttttcaa aggacatact 540
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gctgtacaaa gcttttacgt taacgatagt gatattaatg cacttcgttt tttcaaagac 840
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gatgggttag ctgtatgtac aggttcatgg gactcaacca tgaaaatatg gtctccaggt 1260
tatcaatag 1269

<210> 11
<211> 422
<212> PRT
<213> Saccharomyces cerevisiae

<400> 11
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20 25 30
Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45
His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60
Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80
Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95
Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110
Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125
Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140
Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr

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145                 150                 155                 160
Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
                165                 170                 175
Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
            180                 185                 190
His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
        195                 200                 205
Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val
    210                 215                 220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225                 230                 235                 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
                245                 250                 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
            260                 265                 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
        275                 280                 285
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
    290                 295                 300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305                 310                 315                 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
                325                 330                 335
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
            340                 345                 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
        355                 360                 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
    370                 375                 380
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385                 390                 395                 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
                405                 410                 415
Trp Ser Pro Gly Tyr Gln
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<212> DNA
<213> Artificial Sequence

<220>
<223> ste4-o15

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gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaca caagatacaa 180
gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
ttaaagccaa atatcgtgtt gaaaggccat aataataaaa tctcagattt tcggtggagt 300
cgagattcaa aacgtatttt gagtgcaagt caagatggct ttatgcttat atgggacagt 360
gcttcaggtt taaaacagaa cgctattcca ttagattctc aatgggttct ttcctgcgct 420
atttcgccat cgagtacttt ggtagcaagc gcaggattaa acaataactg taccatttat 480
agagtttcga aagaaaacag agtagcgcaa aacgttgcgt caattttcaa aggacatact 540
tgctatattt ctgacattga atttacagat aacgcacata tattgacagc aagtggggat 600
atgacatgtg ccttgtggga tataccgaaa gcaaagaggg tgagaggata ttctgaccat 660

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ttaggtgatg ttttggcatt agctattcct gaagagccaa acttagaaaa ttcttcgaac 720
acattcgcta gctgtggatc agacgggtat acttacatat gggatagcag atctccgtcc 780
gctgtacaaa gcttttacgt taacgatagt gatattaatg cacttcgttt tttcaaagac 840
gggatgtcga ttgttgcagg aagtgacaat ggtgcgataa atatgtatga tttaaggtcg 900
gactgttcta ttgctacttt ttctcttttt cgaggttatg aagaacgtac ccctaccccc 960
acttatatgg cagctaacat ggagtacaat accgcgcaat cgccacaaac tttaaaatca 1020
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agattgatgt actcatgcta tacagacatt ggttgtgttg tgtgggatgt attaaaagga 1140
gagattgttg gaaaattaga aggtcatggt ggcagagtca ctggtgtgcg ctcgagtcca 1200
gatgggttag ctgtatgtac aggttcatgg gactcaacca tgaaaatatg gtctccaggt 1260
tatcaatag                                                        1269
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<210> 13
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> ste4-o15

<400> 13

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            20                  25                  30
Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
        35                  40                  45
His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
    50                  55                  60
Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65                  70                  75                  80
Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
                85                  90                  95
Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
            100                 105                 110
Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
        115                 120                 125
Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
    130                 135                 140
Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145                 150                 155                 160
Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
                165                 170                 175
Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
            180                 185                 190
His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
        195                 200                 205
Pro Lys Ala Lys Arg Val Arg Gly Tyr Ser Asp His Leu Gly Asp Val
    210                 215                 220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225                 230                 235                 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
                245                 250                 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
            260                 265                 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
        275                 280                 285
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Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
    290                 295                 300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305                 310                 315                 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
                325                 330                 335
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
            340                 345                 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
        355                 360                 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
    370                 375                 380
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385                 390                 395                 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
                405                 410                 415
Trp Ser Pro Gly Tyr Gln
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<210> 14
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> ste4-o17

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gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaca caagatacaa 180
gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
ttaaagccaa atatcgtgtt gaaaggccat aataataaaa tctcagattt tcggtggagt 300
cgagattcaa aacgtatttt gagtgcaagt caagatggct ttatgcttat atgggacagt 360
gcttcaggtt taaaacagaa cgctattcca ttagattctc aatgggttct ttcctgcgct 420
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tgctatattt ctgacattga atttacagat aacgcacata tattgacagc aagtggggat 600
atgacatgtg ccttgtggga tataccgaaa gcaaagaggg tgagagaata ttctgaccat 660
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gctgtacaaa gcttttacgt taacgatagt gatattaatg cacttcgttt tttcaaagac 840
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gactgttcta ttgctacttt ttctcttttt cgaggttatg aagaacgtac ccctacccct 960
acttatatgg cagctaacat ggagtacaat accgcgcaat cgccacaaac tttaaaatca 1020
acaagctcaa gctatctaga caaccaaggc gctgtttctt tagattttag tgcatctgga 1080
agattgatgt actcatgcta tacagacatt ggttgtgttg tgtgggatgt attaaaagga 1140
gagattgttg gaaaattaga aggtcatggt ggcagagtca ctggtgtgcg ctcgagtcca 1200
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<210> 15
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> ste4-o17

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20 25 30
Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45
His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60
Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80
Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95
Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110
Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125
Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140
Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145 150 155 160
Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
165 170 175
Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
180 185 190
His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
195 200 205
Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val
210 215 220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225 230 235 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
245 250 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
260 265 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
275 280 285
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
290 295 300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305 310 315 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
325 330 335
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Ala Val
340 345 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
355 360 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
370 375 380
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385 390 395 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
405 410 415
Trp Ser Pro Gly Tyr Gln

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<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope sequence

<400> 16
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<210> 17
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<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease recognition sequence

<400> 17
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<210> 18
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<212> PRT
<213> Artificial Sequence

<220>
<223> S. cerevisiae Cdc24-m1

<400> 18
Gln Phe Lys Leu Pro Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys
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Lys Ser Ile

<210> 19
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> S. cerevisiae Cdc24-m2

<400> 19
Gln Phe Lys Leu Pro Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys
1 5 10 15
Lys Ser Ile

<210> 20
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> S. cervisiae Cdc24-m3

<400> 20
Gln Phe Lys Leu Pro Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys
 1   5   10   15
Lys Ser Ile

<210> 21
<211> 19
<212> PRT
<213> Saccharomyces cerevisiae

<400> 21
Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys
 1   5   10   15
Lys Ser Ile

<210> 22
<211> 19
<212> PRT
<213> Homo sapien

<400> 22
Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met
 1   5   10   15
Lys Thr Ile

<210> 23
<211> 2535
<212> DNA
<213> Candida albicans

<400> 23
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ttcaataaac caagtactcc caaagaccat ttattctatc gatgtgaatc actaaaacga 180
aaactacaaa aaatccctgg catggaacca tttttgaacc aagctttcaa tcaggctgaa 240
caactcagtg aacaacaagc attggctttg gcacaggaaa gaagcaatgg aaatggacat 300
agtaatggca aacgtcatca atcattagac ggtgccatga atagactttc agttggttct 360
gatagtagtt cgatccaagg ttcattgaca cgaatggcca ccaatgcgtc aacgtcatct 420
ttaatcagtg gtatgccaaa caacaacact ttatttacgt ttactgcagg ggttttacca 480
gctaatatta gtgtcgatcc tgctacccat ctttggaaat tgttccaaca aggggccccc 540
ttttgtgttc ttatcaatca tatccttcct gattcccaaa taccagttgt cagttctgat 600

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gacttgagaa tttgcaaaaa atcagtatat gacttttaa ttgccgtcaa gacacaattg 660
aattttgatg acgagaatat gttcactata tccaatgttt tctccgacaa tgcccaagat 720
ttaatcaaga ttattgatgt cattaataaa ctacttgctg agtactcaga tgctagtgac 780
ctgggtggtg gcgatgaaga tgtaaatatg gatgttcaaa ttaccgatga aagatcaaaa 840
gttttccgag aaattatcga aacagaaaga aaatatgttc aagacttgga actaatgtgt 900
aaataccgtc aagatctaat tgaagccgaa aatttgtctt cagaacaaat tcacttgtta 960
ttcccaaatt taaatgagat tattgatttt caaagacgat tcctcaatgg gttagaatgt 1020
aacatcaatg tacctattag atatcaaaga attggatcag tatttattca tgcttctttg 1080
ggcccttca atgcttatga accttggact ataggacaat tgacggcgat tgatttgatc 1140
aacaaagaag ctgctaattt gaaaaaatcg tcaagtctac ttgatcctgg gtttgaactt 1200
caatcgtata tattaaagcc gatccaaaga ttgtgtaaat acccactttt gttgaaagag 1260
ttaatcaaaa catcaccaga atattcaaaa caggaccccc atggcagctc gtcatcgaca 1320
tcattcaatg aattattggt ggctaaaact gcaatgaaag aattggcaaa tcaagtcaat 1380
gaggcgcaaa gacgagcaga aaatatcgaa catttggaaa aactaaaaga aagagtaggt 1440
aattggcgtg ggtttaattt ggatgctcaa ggagaactat tattccacgg acaagttggg 1500
gttaaagatg ctgaaaatga aaaggaatac gttgcttatc tttttgaaaa aatcgtattt 1560
tttttcacag aaattgatga taccaaaaaa tctgataaac aggaaaagaa gagcaagttt 1620
tcgacaagaa agagatcaac ttcatcaaat cttagttcat cgactactaa tttgttggaa 1680
tcaataaaca attcccgaaa ggataacaca ttgccattgg aattaaaggg aagagtttat 1740
atatcggaga tttataacat ttccgcacca aacactcctg gctcaactct aatcatctca 1800
tggtcaggta gaaaggaaag cggctcattc actttgagat atcgtagtga agaagccaga 1860
aaccaatggg aaaagtgttt acgtgatttg aagactaatg aaatgaataa acaaattcat 1920
aagaagttac gtgattccga cctgtcattt aatactgatg actctgccat atatgattac 1980
acgggtatta gtacgtcacc agtcaatcaa tcaactcaac aacaatacta tgatcatcgg 2040
ggctctcaca gttcccgcca tcactcatcg tcatccactt tgagtatgat gaagaataat 2100
agagttaaat ctggtgattt gagtagaata tcttcaactt caacaacatt agattctttc 2160
agtaacaact tgaatgggtc accaaatacc actaatccat ctttgatgtc ttcagatgcc 2220
accaaaacaa ttccaacatt tgacgttgca attaaattgc tttacaaatc gacagaattg 2280
tcagagccat tgattgtcaa tgcacaaatt gagtataatg acctttttaca gaaaattatc 2340
tcccagatta tcacttcgaa cttggtggca gatgatgtca atattagtcg attgagatat 2400
aaagacgacg aaggagactt tgtgaatttg aattcagatg atgattgggg gttagtgctt 2460
gatatgttaa ccagtgaaga cttttaccaa acatcaagca atgaaaaacg actggtgaca 2520
gtgtgggttt cttga                                                  2535
```

<210> 24
<211> 844
<212> PRT
<213> Candida albicans

<400> 24

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Met Glu His Pro Pro Ala Ala Leu Arg Thr Phe Ser Thr Gln Ser Thr
 1               5                  10                  15
Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile Val Ser
            20                  25                  30
Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr Pro Lys
        35                  40                  45
Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu Gln Lys
    50                  55                  60
Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln Ala Glu
65                  70                  75                  80
Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg Ser Asn
                85                  90                  95
Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp Gly Ala
            100                 105                 110
Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln Gly Ser
        115                 120                 125
Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile Ser Gly
```

```
    130                 135                 140
Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val Leu Pro
145                 150                 155                 160
Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu Phe Gln
                165                 170                 175
Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser
            180                 185                 190
Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
        195                 200                 205
Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp
    210                 215                 220
Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp
225                 230                 235                 240
Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr Ser
                245                 250                 255
Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met Asp Val
            260                 265                 270
Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile Glu Thr
        275                 280                 285
Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr Arg Gln
    290                 295                 300
Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His Leu Leu
305                 310                 315                 320
Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe Leu Asn
                325                 330                 335
Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg Ile Gly
            340                 345                 350
Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr Glu Pro
        355                 360                 365
Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys Glu Ala
    370                 375                 380
Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe Glu Leu
385                 390                 395                 400
Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr Pro Leu
                405                 410                 415
Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys Gln Asp
            420                 425                 430
Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu Val Ala
        435                 440                 445
Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala Gln Arg
    450                 455                 460
Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg Val Gly
465                 470                 475                 480
Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu Phe His
                485                 490                 495
Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr Val Ala
            500                 505                 510
Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp Asp Thr
        515                 520                 525
Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr Arg Lys
    530                 535                 540
Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu Leu Glu
545                 550                 555                 560
Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys
                565                 570                 575
Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr
            580                 585                 590
```

```
Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly
        595                 600                 605
Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu
    610                 615                 620
Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln Ile His
625                 630                 635                 640
Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp Ser Ala
                645                 650                 655
Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln Ser Thr
            660                 665                 670
Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His His
        675                 680                 685
Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val Lys Ser
    690                 695                 700
Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp Ser Phe
705                 710                 715                 720
Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Met
                725                 730                 735
Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys
            740                 745                 750
Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala
        755                 760                 765
Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln Ile Ile
    770                 775                 780
Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu Arg Tyr
785                 790                 795                 800
Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp Asp Trp
                805                 810                 815
Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser
            820                 825                 830
Ser Asn Glu Lys Arg Ser Val Thr Val Trp Val Ser
        835                 840
```

<210> 25
<211> 22
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
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Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser
 1               5                  10                  15
Ile Tyr Asp Phe Ile Leu
            20
```

<210> 26
<211> 22
<212> PRT
<213> Candida albicans

<400> 26
```
Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
 1               5                  10                  15
Val Tyr Asp Phe Leu Ile
            20
```

<210> 27
<211> 854
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27
Met Ala Ile Gln Thr Arg Phe Ala Ser Gly Thr Ser Leu Ser Asp Leu
1 5 10 15
Lys Pro Lys Pro Ser Ala Thr Ser Ile Ser Ile Pro Met Gln Asn Val
20 25 30
Met Asn Lys Pro Val Thr Glu Gln Asp Ser Leu Phe His Ile Cys Ala
35 40 45
Asn Ile Arg Lys Arg Leu Glu Val Leu Pro Gln Leu Lys Pro Phe Leu
50 55 60
Gln Leu Ala Tyr Gln Ser Ser Glu Val Leu Ser Glu Arg Gln Ser Leu
65 70 75 80
Leu Leu Ser Gln Lys Gln His Gln Glu Leu Leu Lys Ser Asn Gly Ala
85 90 95
Asn Arg Asp Ser Ser Asp Leu Ala Pro Thr Leu Arg Ser Ser Ser Ile
100 105 110
Ser Thr Ala Thr Ser Leu Met Ser Met Glu Gly Ile Ser Tyr Thr Asn
115 120 125
Ser Asn Pro Ser Ala Thr Pro Asn Met Glu Asp Thr Leu Leu Thr Phe
130 135 140
Ser Met Gly Ile Leu Pro Ile Thr Met Asp Cys Asp Pro Val Thr Gln
145 150 155 160
Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu Cys Ile Leu Phe Asn
165 170 175
Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu
180 185 190
Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile Leu Gly Cys Lys Lys
195 200 205
His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr Ile Ser Asp Val Phe
210 215 220
Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu Glu Val Val Glu Thr
225 230 235 240
Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser Lys Ser Lys Thr Gln
245 250 255
Gln Ile Met Asn Ala Glu Asn Gln His Arg His Gln Pro Gln Gln Ser
260 265 270
Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile Lys Glu Phe Val Ala
275 280 285
Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile Leu Asp Lys Tyr Arg
290 295 300
Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser Glu Glu Leu Tyr Met
305 310 315 320
Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe Gln Arg Arg Phe Leu
325 330 335
Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro Ser Lys Gln Arg Ile
340 345 350
Gly Ala Leu Phe Met His Ser Lys His Phe Phe Lys Leu Tyr Glu Pro
355 360 365
Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe Leu Ser Ser Thr Leu
370 375 380
His Lys Met Arg Val Asp Glu Ser Gln Arg Phe Ile Ile Asn Asn Lys
385 390 395 400

Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val Gln Arg Leu Cys Arg
405 410 415
Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu Ser Ser Asp Asp Asn
420 425 430
Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile Ser Lys Asn Ile Ala
435 440 445
Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu Asn His Gln Val Val
450 455 460
Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys Gly Tyr Arg Ile Ser
465 470 475 480
Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val Phe Ile Ser Thr Thr
485 490 495
Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu Val Tyr Leu Phe Glu
500 505 510
Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr Lys Lys Ser Ala Ser
515 520 525
Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser Ala Ser Ile Ser Ala
530 535 540
Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His His Ser Tyr His Lys
545 550 555 560
Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile His Leu Ser Ser Ser
565 570 575
Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn Ser Ser Asp Asn Asn
580 585 590
Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys Leu Ser Ala Asn Glu
595 600 605
Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile Met Asn Leu Asn Gln
610 615 620
Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile Thr Trp Glu Ser Ile
625 630 635 640
Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys Asn Glu Glu Thr Arg
645 650 655
Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile His Asp Leu Lys Asn
660 665 670
Glu Gln Phe Lys Ala Arg His His Ser Ser Thr Ser Thr Thr Ser Ser
675 680 685
Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr Thr Thr Met Asn Thr
690 695 700
Pro Asn His His Asn Ser Arg Gln Thr His Asp Ser Met Ala Ser Phe
705 710 715 720
Ser Ser Ser His Met Lys Arg Val Ser Asp Val Leu Pro Lys Arg Arg
725 730 735
Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys Ser Ile Ser Glu Asn
740 745 750
Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu Phe Arg Ile Ser Tyr
755 760 765
Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu Ile Phe Thr Leu Leu
770 775 780
Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile Met Ala Ile Asn Ser
785 790 795 800
Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser Pro Ile Thr Lys Ile
805 810 815
Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val Leu Gly Ser Asp Glu
820 825 830
Asp Trp Asn Val Ala Lys Glu Met Leu Ala Glu Asn Asn Glu Lys Phe
835 840 845
Leu Asn Ile Arg Leu Tyr

850

<210> 28
<211> 837
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28
Ser Gly Thr Ser Leu Ser Asp Leu Lys Pro Lys Pro Ser Ala Thr Ser
1 5 10 15
Ile Ser Ile Pro Met Gln Asn Val Met Asn Lys Pro Val Thr Glu Gln
20 25 30
Asp Ser Leu Phe His Ile Cys Ala Asn Ile Arg Lys Arg Leu Glu Val
35 40 45
Leu Pro Gln Leu Lys Pro Phe Leu Gln Leu Ala Tyr Gln Ser Ser Glu
50 55 60
Val Leu Ser Glu Arg Gln Ser Leu Leu Leu Ser Gln Lys Gln His Gln
65 70 75 80
Glu Leu Leu Lys Ser Asn Gly Ala Asn Arg Asp Ser Ser Asp Leu Ala
85 90 95
Pro Thr Leu Arg Ser Ser Ser Ile Ser Thr Ala Thr Ser Leu Met Ser
100 105 110
Met Glu Gly Ile Ser Tyr Thr Asn Ser Asn Pro Ser Ala Thr Pro Asn
115 120 125
Met Glu Asp Thr Leu Leu Thr Phe Ser Met Gly Ile Leu Pro Ile Thr
130 135 140
Met Asp Cys Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly
145 150 155 160
Ala Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu
165 170 175
Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr
180 185 190
Asp Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu
195 200 205
Leu Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val
210 215 220
Lys Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile
225 230 235 240
Phe Pro Ser Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln
245 250 255
His Arg His Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val
260 265 270
Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp
275 280 285
Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu
290 295 300
Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
305 310 315 320
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
325 330 335
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
340 345 350
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
355 360 365
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
370 375 380

```
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
385                 390                 395                 400
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
                405                 410                 415
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
            420                 425                 430
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
        435                 440                 445
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
    450                 455                 460
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe
465                 470                 475                 480
Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg
                485                 490                 495
Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu
            500                 505                 510
Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser
        515                 520                 525
Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly
    530                 535                 540
Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser
545                 550                 555                 560
Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser
                565                 570                 575
Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser
            580                 585                 590
Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
        595                 600                 605
Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
    610                 615                 620
Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
625                 630                 635                 640
Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
                645                 650                 655
Gln Leu Ile His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His
            660                 665                 670
Ser Ser Thr Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met
        675                 680                 685
Ser Pro Thr Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln
    690                 695                 700
Thr His Asp Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val
705                 710                 715                 720
Ser Asp Val Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser
                725                 730                 735
Glu Ile Lys Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser
            740                 745                 750
Ser Ile Leu Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser
        755                 760                 765
Ser Ser Glu Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp
    770                 775                 780
Asp Leu Ile Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn
785                 790                 795                 800
Asn Ile Ser Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp
                805                 810                 815
Phe Val Val Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu Met
            820                 825                 830
Leu Ala Glu Asn Asn
```

835

<210> 29
<211> 813
<212> PRT
<213> Candida albicans

<400> 29

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Ser Thr Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile
 1               5                  10                  15
Val Ser Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr
            20                  25                  30
Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu
        35                  40                  45
Gln Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln
    50                  55                  60
Ala Glu Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg
65                  70                  75                  80
Ser Asn Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp
                85                  90                  95
Gly Ala Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln
            100                 105                 110
Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile
        115                 120                 125
Ser Gly Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val
    130                 135                 140
Leu Pro Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu
145                 150                 155                 160
Phe Gln Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro
                165                 170                 175
Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
            180                 185                 190
Lys Ser Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe
        195                 200                 205
Asp Asp Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala
    210                 215                 220
Gln Asp Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu
225                 230                 235                 240
Tyr Ser Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met
                245                 250                 255
Asp Val Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile
            260                 265                 270
Glu Thr Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr
        275                 280                 285
Arg Gln Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His
    290                 295                 300
Leu Leu Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe
305                 310                 315                 320
Leu Asn Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg
                325                 330                 335
Ile Gly Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr
            340                 345                 350
Glu Pro Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys
        355                 360                 365
Glu Ala Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe
    370                 375                 380
```

```
Glu Leu Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr
385                 390                 395                 400
Pro Leu Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys
                405                 410                 415
Gln Asp Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu
            420                 425                 430
Val Ala Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala
        435                 440                 445
Gln Arg Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg
    450                 455                 460
Val Gly Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu
465                 470                 475                 480
Phe His Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr
                485                 490                 495
Val Ala Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp
            500                 505                 510
Asp Thr Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr
        515                 520                 525
Arg Lys Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu
    530                 535                 540
Leu Glu Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu
545                 550                 555                 560
Leu Lys Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro
                565                 570                 575
Asn Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu
            580                 585                 590
Ser Gly Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln
        595                 600                 605
Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln
    610                 615                 620
Ile His Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp
625                 630                 635                 640
Ser Ala Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln
                645                 650                 655
Ser Thr Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg
            660                 665                 670
His His Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val
        675                 680                 685
Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp
    690                 695                 700
Ser Phe Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser
705                 710                 715                 720
Leu Met Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala
                725                 730                 735
Ile Lys Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val
            740                 745                 750
Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln
        755                 760                 765
Ile Ile Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu
    770                 775                 780
Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp
785                 790                 795                 800
Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp
                805                 810
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<210> 30

<211> 684
<212> PRT
<213> Saccharomyces cerevisiae

<400> 30
Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu
1 5 10 15
Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile
20 25 30
Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile
35 40 45
Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr
50 55 60
Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu
65 70 75 80
Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser
85 90 95
Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln His Arg His
100 105 110
Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile
115 120 125
Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile
130 135 140
Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser
145 150 155 160
Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe
165 170 175
Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro
180 185 190
Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys His Phe Phe
195 200 205
Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe
210 215 220
Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser Gln Arg Phe
225 230 235 240
Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val
245 250 255
Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu
260 265 270
Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile
275 280 285
Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu
290 295 300
Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys
305 310 315 320
Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val
325 330 335
Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu
340 345 350
Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr
355 360 365
Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser
370 375 380
Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His
385 390 395 400
His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile
405 410 415

```
His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn
            420                 425                 430
Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys
        435                 440                 445
Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile
    450                 455                 460
Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile
465                 470                 475                 480
Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys
                485                 490                 495
Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile
            500                 505                 510
His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His Ser Ser Thr
        515                 520                 525
Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr
    530                 535                 540
Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln Thr His Asp
545                 550                 555                 560
Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val Ser Asp Val
                565                 570                 575
Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys
            580                 585                 590
Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu
        595                 600                 605
Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu
    610                 615                 620
Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile
625                 630                 635                 640
Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser
                645                 650                 655
Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val
            660                 665                 670
Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu
        675                 680
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<210> 31
<211> 742
<212> PRT
<213> Schizosaccharomyces pombe

<400> 31

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Asp Pro Val Thr Glu Ile Trp Leu Phe Cys Arg Leu Gly Tyr Pro Leu
 1               5                  10                  15
Cys Ala Leu Phe Asn Cys Leu Pro Val Lys Gln Lys Leu Glu Val Asn
            20                  25                  30
Ser Ser Val Ser Leu Glu Asn Thr Asn Val Cys Lys Ala Ser Leu Tyr
        35                  40                  45
Arg Phe Met Leu Met Cys Lys Asn Glu Leu Gly Leu Thr Asp Ala Ala
    50                  55                  60
Leu Phe Ser Ile Ser Glu Ile Tyr Lys Pro Ser Thr Ala Pro Leu Val
65                  70                  75                  80
Arg Ala Leu Gln Thr Ile Glu Leu Leu Leu Lys Lys Tyr Glu Val Ser
                85                  90                  95
Asn Thr Thr Lys Ser Ser Ser Thr Pro Ser Pro Ser Thr Asp Asp Asn
            100                 105                 110
Val Pro Thr Gly Thr Leu Asn Ser Leu Ile Ala Ser Gly Arg Arg Val
```

```
        115                 120                 125
Thr Ala Glu Leu Tyr Glu Thr Glu Leu Lys Tyr Ile Gln Asp Leu Glu
    130                 135                 140
Tyr Leu Ser Asn Tyr Met Val Ile Leu Gln Gln Lys Gln Ile Leu Ser
145                 150                 155                 160
Gln Asp Thr Ile Leu Ser Ile Phe Thr Asn Leu Asn Glu Ile Leu Asp
                165                 170                 175
Phe Gln Arg Arg Phe Leu Val Gly Leu Glu Met Asn Leu Ser Leu Pro
            180                 185                 190
Val Glu Glu Gln Arg Leu Gly Ala Leu Phe Ile Ala Leu Glu Glu Gly
        195                 200                 205
Phe Ser Val Tyr Gln Val Phe Cys Thr Asn Phe Pro Asn Ala Gln Gln
    210                 215                 220
Leu Ile Ile Asp Asn Gln Asn Gln Leu Leu Lys Val Ala Asn Leu Leu
225                 230                 235                 240
Glu Pro Ser Tyr Glu Leu Pro Ala Leu Leu Ile Lys Pro Ile Gln Arg
                245                 250                 255
Ile Cys Lys Tyr Pro Leu Leu Leu Asn Gln Leu Leu Lys Gly Thr Pro
            260                 265                 270
Ser Gly Tyr Gln Tyr Glu Glu Glu Leu Lys Gln Gly Met Ala Cys Val
        275                 280                 285
Val Arg Val Ala Asn Gln Val Asn Glu Thr Arg Arg Ile His Glu Asn
    290                 295                 300
Arg Asn Ala Ile Ile Glu Leu Glu Gln Arg Val Ile Asp Trp Lys Gly
305                 310                 315                 320
Tyr Ser Leu Gln Tyr Phe Gly Gln Leu Leu Val Trp Asp Val Val Asn
                325                 330                 335
Val Cys Lys Ala Asp Ile Glu Arg Glu Tyr His Val Tyr Leu Phe Glu
            340                 345                 350
Lys Ile Leu Leu Cys Cys Lys Glu Met Ser Thr Leu Lys Arg Gln Ala
        355                 360                 365
Arg Ser Ile Ser Met Asn Lys Lys Thr Lys Arg Leu Asp Ser Leu Gln
    370                 375                 380
Leu Lys Gly Arg Ile Leu Thr Ser Asn Ile Thr Thr Val Val Pro Asn
385                 390                 395                 400
His His Met Gly Ser Tyr Ala Ile Gln Ile Phe Trp Arg Gly Asp Pro
                405                 410                 415
Gln His Glu Ser Phe Ile Leu Lys Leu Arg Asn Glu Glu Ser His Lys
            420                 425                 430
Leu Trp Met Ser Val Leu Asn Arg Leu Leu Trp Lys Asn Glu His Gly
        435                 440                 445
Ser Pro Lys Asp Ile Arg Ser Ala Ala Ser Thr Pro Ala Asn Pro Val
    450                 455                 460
Tyr Asn Arg Ser Ser Ser Gln Thr Ser Lys Gly Tyr Asn Ser Ser Asp
465                 470                 475                 480
Tyr Asp Leu Leu Arg Thr His Ser Leu Asp Glu Asn Val Asn Ser Pro
                485                 490                 495
Thr Ser Ile Ser Ser Pro Ser Ser Lys Ser Ser Pro Phe Thr Lys Thr
            500                 505                 510
Thr Ser Lys Asp Thr Lys Ser Ala Thr Thr Thr Asp Glu Arg Pro Ser
        515                 520                 525
Asp Phe Ile Arg Leu Asn Ser Glu Glu Ser Val Gly Thr Ser Ser Leu
    530                 535                 540
Arg Thr Ser Gln Thr Thr Ser Thr Ile Val Ser Asn Asp Ser Ser Ser
545                 550                 555                 560
Thr Ala Ser Ile Pro Ser Gln Ile Ser Arg Ile Ser Gln Val Asn Ser
                565                 570                 575
```

```
Leu Leu Asn Asp Tyr Asn Tyr Asn Arg Gln Ser His Ile Thr Arg Val
            580                 585                 590
Tyr Ser Gly Thr Asp Asp Gly Ser Ser Val Ser Ile Phe Glu Asp Thr
        595                 600                 605
Ser Ser Ser Thr Lys Gln Lys Ile Phe Asp Gln Pro Thr Thr Asn Asp
    610                 615                 620
Cys Asp Val Met Arg Pro Arg Gln Tyr Ser Tyr Ser Ala Gly Met Lys
625                 630                 635                 640
Ser Asp Gly Ser Leu Leu Pro Ser Thr Lys His Thr Ser Leu Ser Ser
                645                 650                 655
Ser Ser Thr Ser Thr Ser Leu Ser Val Arg Asn Thr Thr Asn Val Lys
            660                 665                 670
Ile Arg Leu Arg Leu His Glu Val Ser Leu Val Leu Val Val Ala His
        675                 680                 685
Asp Ile Thr Phe Asp Glu Leu Leu Ala Lys Val Glu His Lys Ile Lys
    690                 695                 700
Leu Cys Gly Ile Leu Lys Gln Ala Val Pro Phe Arg Val Arg Leu Lys
705                 710                 715                 720
Tyr Val Asp Glu Asp Gly Asp Phe Ile Thr Ile Thr Ser Asp Glu Asp
                725                 730                 735
Val Leu Met Ala Phe Glu
            740
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<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 12
<223> n = A,T,C or G

<221> misc_feature
<222> 3, 7, 18
<223> r = A or G

<221> misc_feature
<222> 6, 15
<223> y = C or T

<221> misc_feature
<222> 9
<223> k = G or T

<221> misc_feature
<222> 12
<223> n = A,T,C or G

<400> 32
aartayrtkc angayttrga 20

<210> 33
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 13
<223> n = A,T,C or G

<221> misc_feature
<222> 1, 10, 15, 16
<223> r = A or G

<221> misc_feature
<222> 7
<223> y = C or T

<221> misc_feature
<222> 13
<223> n = A,T,C or G

<400> 33
rattttytcr aanarrta 18

<210> 34
<211> 76
<212> PRT
<213> Candida albicans

<400> 34
Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15
Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30
Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
35 40 45
Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60
Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr
65 70 75

<210> 35
<211> 19
<212> PRT
<213> Candida albicans

<400> 35
Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
1 5 10 15
Lys Ser Val

<210> 36
<211> 73

<212> PRT
<213> Candida albicans

<400> 36
Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
 1   5   10   15
Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
            20   25   30
Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
        35   40   45
Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
    50   55   60
Ile Ile Asp Val Ile Asn Lys Leu Leu
65   70

<210> 37
<211> 73
<212> PRT
<213> Saccharomyces cerevisiae

<400> 37
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
 1   5   10   15
Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
            20   25   30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
        35   40   45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
    50   55   60
Val Leu Glu Val Val Glu Thr Leu Met
65   70